SEQUENCE LISTING

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Biosite Diagnostics

<120> Diagnostic Assays for Detection of Cryptosporidium

parvum

<130> 014907-001900US

<140> 09/158,180

<141> 1998-09-21

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 1446

<212> DNA

<213> Cryptosporidium parvum

<220>

<221> CDS

<222> (1)..(1446)

<223> C. parvum protein disulfide isomerase (PDI) cDNA

of Applicants

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Met Ile Gly Ile Arg Ser Leu Val Ser Ala Ala Phe Leu Gly Phe Ser
 1               5                  10                 15


tgt ctc tcc aag gta gtc ttg ggt gga gat gaa gct cac ttc att tca    96
Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser
                20                  25                 30


gaa cac att act tcc tta act tcc tcc aac ttc gaa gac ttc att aag    144
Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys
            35                  40                 45


agc aag gaa cac gta att gtt act ttc ttt gcc cca tgg tgc ggc cat    192
Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His
        50                  55                  60


tgt act gct tta gag cca gaa ttc aag gca aca tgc gct gaa atc tca    240
Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser
65                  70                  75                  80


aag ctc tct ccc cca gta cac tgt ggc agt gtt gat gca act gaa aat    288
Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn
                85                  90                  95


atg gag ctt gca caa caa tat ggt gtg agc gga tac cca acc atc aaa    336
Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys
            100                 105                 110
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ttc ttc agt ggt att gac agt gtt cag aac tat tca gga gca aga agc   384
Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser
       115   120   125

aag gat gca ttc atc aag tat att aag aag ttg acc gga cca gca gtc   432
Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val
       130   135   140

caa gtt gct gaa tca gaa gaa gct atc aag aca atc ttc gct tct tct   480
Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser
145   150   155   160

tct tca gcc ttt gtt gga aga ttc acc tct aag gac tca gct gag tat   528
Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr
           165   170   175

gct gtc ttc gag aag gtt gct agt ggt cac cgc gag cac aac tat gct   576
Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala
           180   185   190

ttc att gct ttc ttc caa gaa ggt gaa caa aag ctc gag gta tta cac   624
Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His
       195   200   205

aag gac gag gag cca gtt tct ctc cca atg cca aag act gtt gaa gag   672
Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu
       210   215   220

ttg gag gcc aag ata tcc ata atg aat gta cca ttg ttc tct gca att   720
Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile
225   230   235   240

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agt gct gag aac tac tcc ctc tat atg tca aga gaa ggt tat act gcc    768
Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala
                245                 250                 255


tgg ttc tgt ggt act aac gag gac ttc gcc aag tat gct tca aac att    816
Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile
                260                 265                 270


aga aag gtt gca gct gat tac aga gaa aag tat gcc ttt gtt ttc ctt    864
Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu
                275                 280                 285


gat act gag caa ttt ggt tcc cat gct act caa cat ctc tta att gag    912
Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu
            290                 295                 300


aaa ttc cca ggt ttg gtt atc caa agt gtc aat gtt cca tca att aga    960
Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg
305                 310                 315                 320


tac atg tat ggt cca gct aaa ttc gac tct gtt gag cca tta aag gaa   1008
Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu
                325                 330                 335


ttt atg aag caa gtt tct gaa ggc aag cac gaa ctc agc att aag tct   1056
Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser
                340                 345                 350


gag cca atc cca gct gag caa tct ggt cca gtc act gtt gtt gtt ggt   1104
Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly
                355                 360                 365
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aag acc ttc gaa gaa att gtt ttc aga agt gac aag gat gtt ctt ttg      1152
Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu
        370             375             380


gaa atc tat gcc caa tgg tgt gga cac tgt aag aac ctc gag cca atc      1200
Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile
385             390             395             400


tac aac caa ctc ggc gaa gag tac aag gac aac gac aag gtt gtg att      1248
Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile
                405             410             415


gca aag atc aat gga cca caa aac gat atc cca tat gaa ggt ttc agt      1296
Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser
                420             425             430


cca aga gcc ttc cca act atc ttg ttc gtc aag gcc gga act aga acc      1344
Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr
                435             440             445


cca att cct tat gat gga aag aga act gtt gag gcc ttc aag gaa ttc      1392
Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe
        450             455             460


atc agt gaa cat tct tcc ttc cct caa gaa aag gaa tct cgt gac gaa      1440
Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu
465             470             475             480


ctc taa                                                              1446
Leu
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<210> 2

<211> 481

<212> PRT

<213> Cryptosporidium parvum

<400> 2

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1   5   10   15

Cys Leu Ser Lys Val Val Leu Gly Gly Asp Glu Ala His Phe Ile Ser

                20   25   30

Glu His Ile Thr Ser Leu Thr Ser Ser Asn Phe Glu Asp Phe Ile Lys

            35   40   45

Ser Lys Glu His Val Ile Val Thr Phe Phe Ala Pro Trp Cys Gly His

        50   55   60

Cys Thr Ala Leu Glu Pro Glu Phe Lys Ala Thr Cys Ala Glu Ile Ser

65   70   75   80

Lys Leu Ser Pro Pro Val His Cys Gly Ser Val Asp Ala Thr Glu Asn

                85   90   95

Met Glu Leu Ala Gln Gln Tyr Gly Val Ser Gly Tyr Pro Thr Ile Lys

                100   105   110

Phe Phe Ser Gly Ile Asp Ser Val Gln Asn Tyr Ser Gly Ala Arg Ser

            115   120   125

Lys Asp Ala Phe Ile Lys Tyr Ile Lys Lys Leu Thr Gly Pro Ala Val
   130   135   140

Gln Val Ala Glu Ser Glu Glu Ala Ile Lys Thr Ile Phe Ala Ser Ser
145   150   155   160

Ser Ser Ala Phe Val Gly Arg Phe Thr Ser Lys Asp Ser Ala Glu Tyr
           165   170   175

Ala Val Phe Glu Lys Val Ala Ser Gly His Arg Glu His Asn Tyr Ala
         180   185   190

Phe Ile Ala Phe Phe Gln Glu Gly Glu Gln Lys Leu Glu Val Leu His
      195   200   205

Lys Asp Glu Glu Pro Val Ser Leu Pro Met Pro Lys Thr Val Glu Glu
    210   215   220

Leu Glu Ala Lys Ile Ser Ile Met Asn Val Pro Leu Phe Ser Ala Ile
225   230   235   240

Ser Ala Glu Asn Tyr Ser Leu Tyr Met Ser Arg Glu Gly Tyr Thr Ala
          245   250   255

Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn Ile
         260   265   270

Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe Leu
    275   280   285

Asp Thr Glu Gln Phe Gly Ser His Ala Thr Gln His Leu Leu Ile Glu
    290   295   300

Lys Phe Pro Gly Leu Val Ile Gln Ser Val Asn Val Pro Ser Ile Arg
305   310   315   320

Tyr Met Tyr Gly Pro Ala Lys Phe Asp Ser Val Glu Pro Leu Lys Glu
                325   330   335

Phe Met Lys Gln Val Ser Glu Gly Lys His Glu Leu Ser Ile Lys Ser
            340   345   350

Glu Pro Ile Pro Ala Glu Gln Ser Gly Pro Val Thr Val Val Val Gly
            355   360   365

Lys Thr Phe Glu Glu Ile Val Phe Arg Ser Asp Lys Asp Val Leu Leu
    370   375   380

Glu Ile Tyr Ala Gln Trp Cys Gly His Cys Lys Asn Leu Glu Pro Ile
385   390   395   400

Tyr Asn Gln Leu Gly Glu Glu Tyr Lys Asp Asn Asp Lys Val Val Ile
                405   410   415

Ala Lys Ile Asn Gly Pro Gln Asn Asp Ile Pro Tyr Glu Gly Phe Ser
            420   425   430

Pro Arg Ala Phe Pro Thr Ile Leu Phe Val Lys Ala Gly Thr Arg Thr
            435   440   445

Pro Ile Pro Tyr Asp Gly Lys Arg Thr Val Glu Ala Phe Lys Glu Phe

    450   455   460

Ile Ser Glu His Ser Ser Phe Pro Gln Glu Lys Glu Ser Arg Asp Glu

465   470   475   480

Leu

<210> 3

<211> 32

<212> PRT

<213> Cryptosporidium parvum

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> 32 amino acid region for C. parvum protein

      disulfide isomerase (PDI) of Applicants differing

      from Blunt et al. (1996) Gene 181:221-223; GenBank

      Accession No. U48261

<400> 3

Ala Trp Phe Cys Gly Thr Asn Glu Asp Phe Ala Lys Tyr Ala Ser Asn

 1   5   10   15

Ile Arg Lys Val Ala Ala Asp Tyr Arg Glu Lys Tyr Ala Phe Val Phe

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<210> 4

<211> 41

<212> PRT

<213> Cryptosporidium parvum

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> positions 250-290 of C. parvum protein disulfide

isomerase (PDI) according to Blunt et al. (1996)

Gene 181:221-223; GenBank Accession No. U48261

<220>

<221> PEPTIDE

<222> (7)..(38)

<223> 32 amino acid region of C. parvum protein

disulfide isomerase (PDI) of Blunt et al. that

differs from that of Applicant PDI

<400> 4

Ser Arg Glu Gly Tyr Thr Pro Gly Ser Val Val Leu Thr Arg Thr Ser

1   5   10   15

Pro Ser Met Leu Gln Thr Leu Glu Arg Leu Gln Leu Ile Thr Glu Lys

            20   25   30

Ser Met Pro Leu Phe Ser Leu Asp Thr

        35   40

<210> 5

<211> 41

<212> PRT

<213> Cryptosporidium parvum

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> positions 250-290 (numbering convention used by

Blunt et al.) of C. parvum protein disulfide

isomerase (PDI) of the Applicants

<220>

<221> PEPTIDE

<222> (7)..(38)

<223> 32 amino acid region of C. parvum protein

disulfide isomerase (PDI) from Applicants that

differs from Blunt et al. PDI

<400> 5

Ser Arg Glu Gly Tyr Thr Ala Trp Phe Cys Gly Thr Asn Glu Asp Phe

1   5   10   15

Ala Lys Tyr Ala Ser Asn Ile Arg Lys Val Ala Ala Asp Tyr Arg Glu

            20   25   30

Lys Tyr Ala Phe Val Phe Leu Asp Thr

        35   40

<210> 6

<211> 23

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer A

<400> 6

gtaaaacgac ggccagtgaa ttg   23

<210> 7

<211> 54

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer B

<400> 7

acccgttttt ttggatggag tgaaacgatg atcggaattc gtagcttggt ttca   54

<210> 8

<211> 89

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer C

<400> 8

gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atggtgatgg 60

tgatggagtt cgtcacgaga ttccttttc   89

<210> 9

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer D

<400> 9

tccaaggtag tcttgggtgg   20

<210> 10

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer E

<400> 10

aagctctctc ccccagtaca   20

<210> 11

<211> 20

<212> DNA

<213> Cryptosporidium parvum

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<223> primer F

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gcagtccaag ttgctgaatc   20

<210> 12

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer G

<400> 12

ctcgaggtat tacacaagga   20

<210> 13

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer H

<400> 13

ccaagtatgc ttcaaacatt   20

<210> 14

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer I

<400> 14

ttcgactctg ttgagccatt   20

<210> 15

<211> 21

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer J

<400> 15

tgtggacact gtaagaacct c   21

<210> 16

<211> 18

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer K

<400> 16

gaggatgacg atgagcgc   18

<210> 17

<211> 21

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer L

<400> 17

gcaactctct actgtttctc c   21

<210> 18

<211> 20

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer M

<400> 18

tcgctgccca accagccatg   20

<210> 19

<211> 75

<212> DNA

<213> Cryptosporidium parvum

<220>

<223> primer N

<400> 19

gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atggtgatgg 60

tgatgacaat ccctg   75